Past and Future Research

Martin Hemberg

PhD Research

- Solutions and analyses of the chemical master equation with application to gene regulation

  - Mathematical proof of a Monte Carlo algorithm

  - Models of qPCR and FACS data from single cells

Post-doc Research

- Analysis of ChIP-Seq and RNA-Seq data
  - Discovery of a novel class of RNA at enhancers
  - Accounting of transcription and TF binding sites

Future Work: Organizing principles of the genome

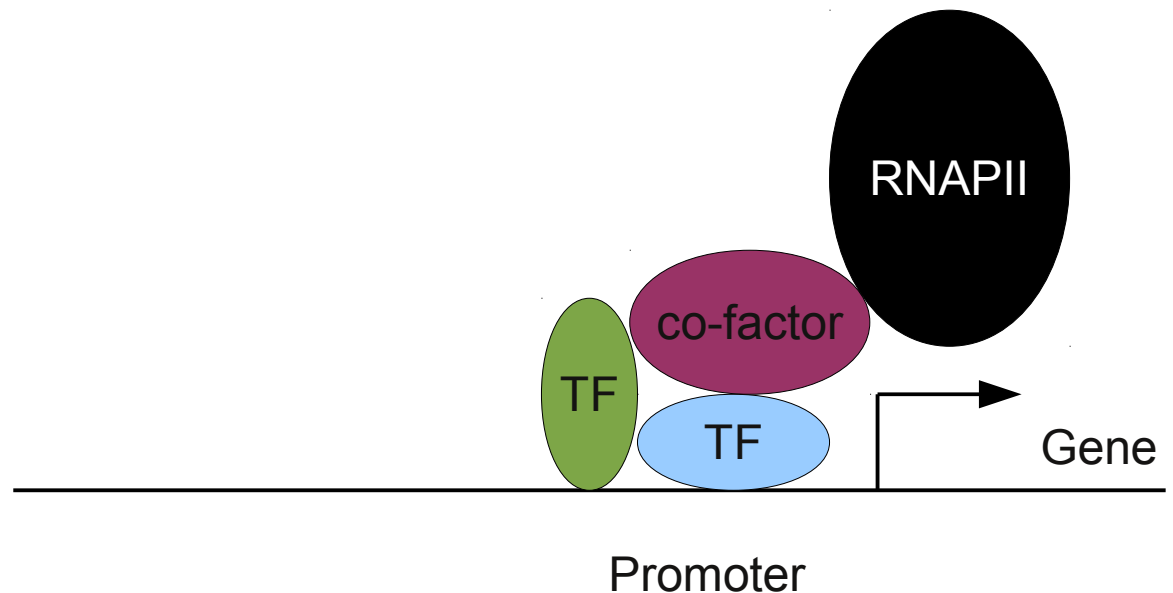- Use genome-wide data to develop systems biology and biophysical models
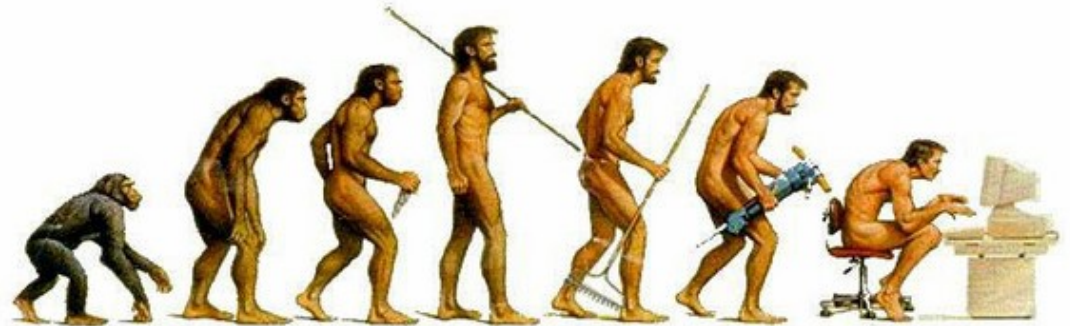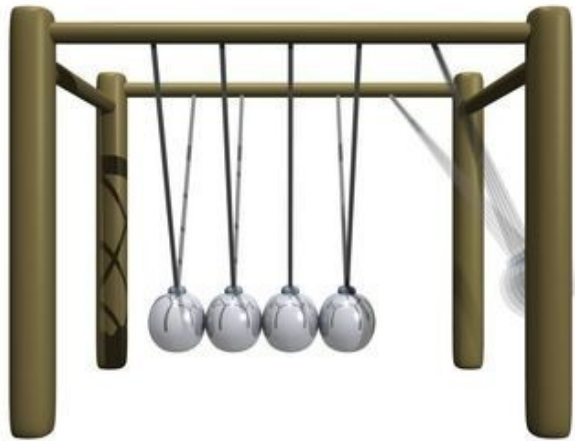
Relevance to Bioengineering

- Quantitative models for molecular biology
- Understand genomic design principles

Can biophysical models improve our understanding of TF binding and transcription?
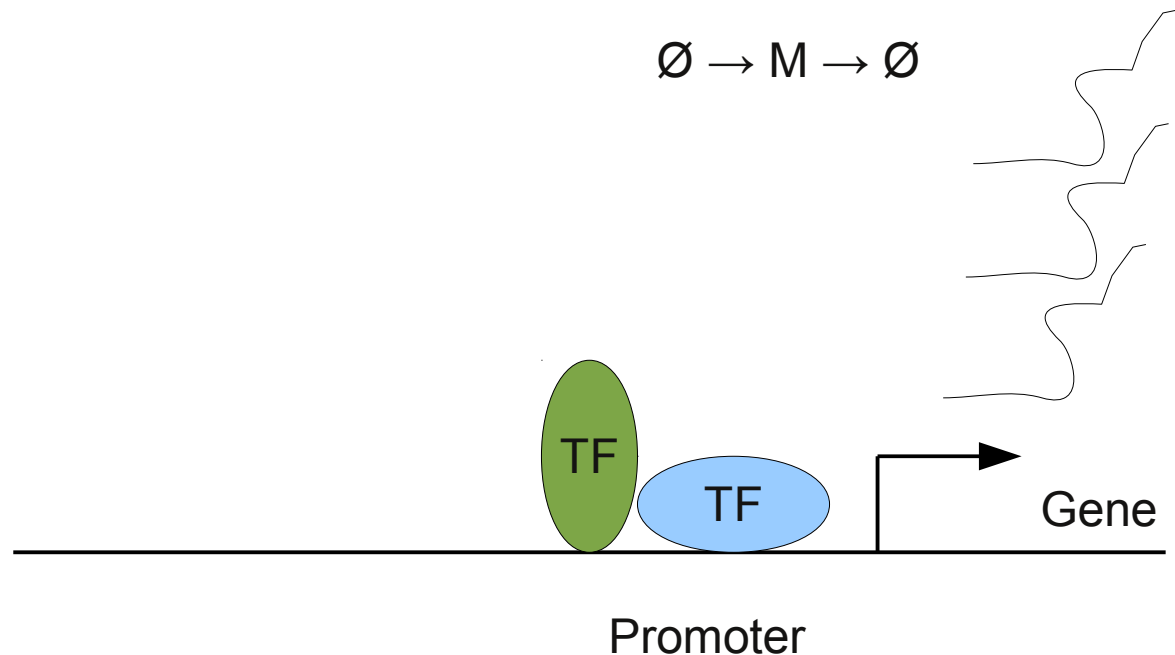
- Use ChIP-Seq to test and compare biophysical models of TF binding

Can we develop a mathematical framework that accounts for parametric noise and robustness?

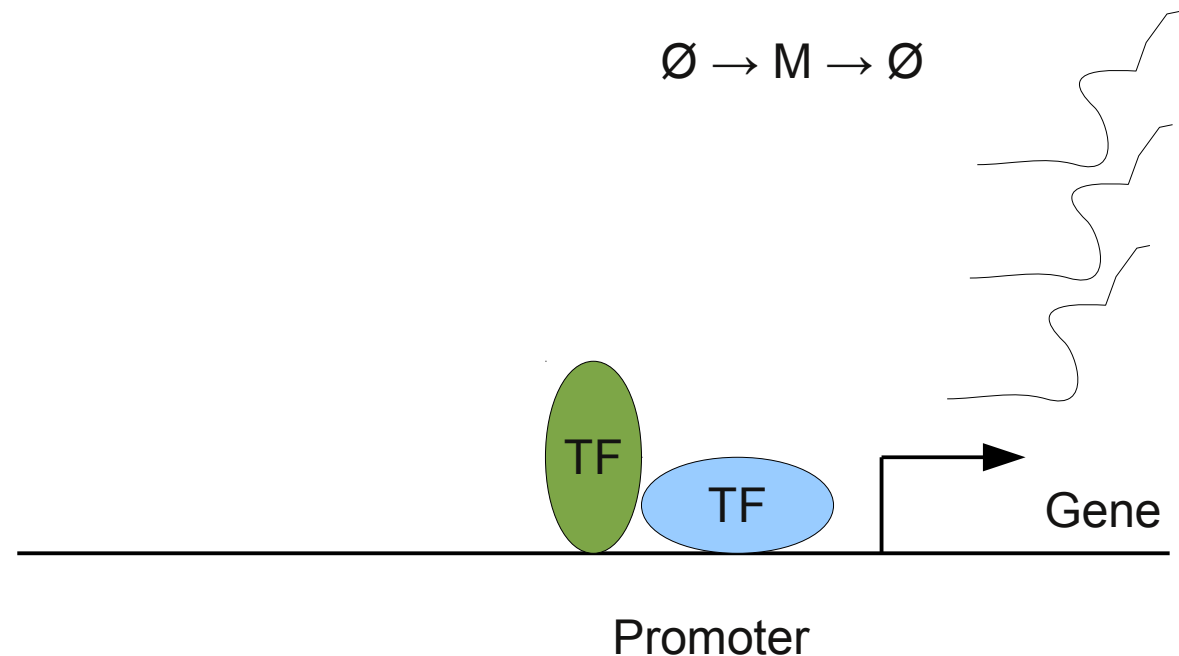- Molecular noise does not fit observations

$$dP(m)/dt = kP(m-1) + P(m+1) - (m+k)P(m)$$

$$\varnothing \rightarrow M \rightarrow \varnothing$$

TF

TF

Gene

Promoter

Can we develop a mathematical framework that accounts for parametric noise and robustness?

- Molecular noise does not fit observations

- Incorporate parametric noise

$$dP(m)/dt = kP(m-1) + P(m+1) - (m+k)P(m)$$

$$\emptyset \rightarrow M \rightarrow \emptyset$$

TF

TF

Gene

Promoter

What is the impact on the phenotype from gene expression noise?

- RNA-Seq for single cells

- Global view of noise in
  gene expression

 - Pathways

  - Proximity

  - Cell-types

  - Propagation

Tracing the Derivation of Embryonic Stem Cells from the Inner Cell Mass by Single-Cell RNA-Seq Analysis

Fuchou Tang,[1,3] Catalin Barbacioru,[2] Siqin Bao,[1] Caroline Lee,[1] Ellen Nordman,[2] Xiaohui Wang,[2] Kaiqin Lao,[2,*] and M. Azim Surani[1,*]

What is the structure of ncRNAs?

- Many classes of novel RNAs

- Structure → function

  - Structural motifs

  - Families of ncRNAs

......ACGUCCAAAUUCCCUAGGCUCAAGGCAUUCGAUCGGGAUUAUA.....→
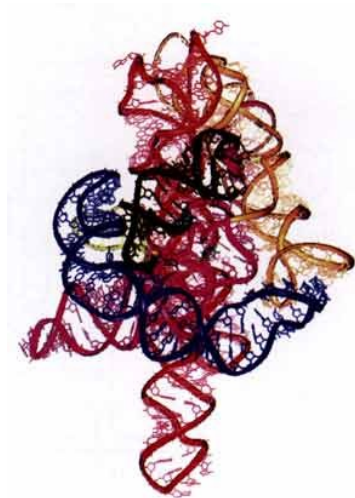
Can we learn more about enhancers by comparing their locations in multiple species?

- Conservation of the genomic context of enhancers
- Evolutionary trajectories of enhancers and promoters